

10/520333

atg gcc aca cag gga caa cgc gtc aac tgg gga gat gaa cct tcc aaa	48
Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser Lys	
aga cgt gat cgt tct aac tct cgt ggt cgg aag aat aat ata cct	96
Arg Arg Asp Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asn Ile Pro	
ctt tca ttc ttc aac ccc acc acc ctc gaa caa gga gct aaa ttt tgg	144
Leu Ser Phe Phe Asn Pro Thr Thr Leu Glu Gln Gly Ala Lys Phe Trp	
tat gta tgt cag aga gac ttt gtt ccc aag gga ata ggt aat aag gat	192
Tyr Val Cys Pro Arg Asp Phe Val Pro Lys Gly Ile Gly Asn Lys Asp	
caa caa att ggt tat tgg aac aga cag gcg cgc ttt cgc att gtc aag	240
Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ala Arg Phe Arg Ile Val Lys	
ggt cag cgt aag gaa ctc cct gag aga tgg ttt ttc tat ttc tta ggt	288
Gly Gln Arg Lys Glu Leu Pro Glu Arg Trp Phe Phe Tyr Phe Leu Gly	
aca gga cct cat gct gat gct aaa ttt aaa gat aag att gat gga gtc	336
Thr Gly Pro His Ala Asp Ala Lys Phe Lys Asp Lys Ile Asp Gly Val	
ttc tgg gtt gca aag gat ggt gcc atg aac aag cca aca tca ctt gcc	384
Phe Trp Val Ala Lys Asp Gly Ala Met Asn Lys Pro Thr Ser Leu Gly	
act cgt gga acc aac aat gaa tcc gaa cca ttg aga ttt gat ggt aag	432
Thr Arg Gly Thr Asn Asn Glu Ser Glu Pro Leu Arg Phe Asp Gly Lys	
ata cca cca caa ttc cag ctt gaa gta aac cgt tct agg aat aat tca	480
Ile Pro Pro Gln Phe Gln Leu Glu Val Asn Arg Ser Arg Asn Asn Ser	
agg tct ggt tct cag tct aga tct gcc tca aga aac agg tct caa tcc	528
Arg Ser Gly Ser Gln Ser Arg Ser Gly Ser Arg Asn Arg Ser Gln Ser	
agg gga aga caa caa tcc aat aac cag aat act aat gtt gag gat aca	576
Arg Gly Arg Gln Gln Ser Asn Asn Gln Asn Thr Asn Val Glu Asp Thr	
att gta gct gtg ctt cag aaa tta ggt gtt act gac aag caa agg tca	624
Ile Val Ala Val Leu Gln Lys Leu Gly Val Thr Asp Lys Gln Arg Ser	
cgt tct aaa tct aga gac cgt agt gac tct aaa tct aga gac aca aca	672
Arg Ser Lys Ser Arg Asp Arg Ser Asp Ser Lys Ser Arg Asp Thr Thr	
cct aaa aac gcc aac aaa cac acc tgg aag aaa act gca ggt aag ggt	720
Pro Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly	
gat gtg aca aat ttc ttt ggt gct aga agt gct tcg gct aac ttt ggt	768
Asp Val Thr Asn Phe Phe Gly Ala Arg Ser Ala Ser Ala Asn Phe Gly	
gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac cct cag	816
Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr Pro Gln	
ata gcc gaa tgc gtt cca tca gta tct agc gtg ctc ttc ggt agt caa	864
Ile Ala Glu Cys Val Pro Ser Val Ser Ser Val Leu Phe Gly Ser Gln	
tgg tcc gct gaa gaa gct gga gat caa gtg aaa gtc aca ctt act cac	912
Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val Thr Leu Thr His	
acc tac tac ctg cca aaa ggt gat gcc aaa acc agt caa ttc cta gaa	960
Thr Tyr Tyr Leu Pro Lys Gly Asp Ala Lys Thr Ser Gln Phe Leu Glu	
cag att gac gct tac aag cgc cct tca caa gta gct aag gaa cag agg	1008
Gln Ile Asp Ala Tyr Lys Arg Pro Ser Gln Val Ala Lys Glu Gln Arg	
aaa cca aag cct cgc tct aag tct gct gat aag aag cct gag gaa ttg	1056
Lys Pro Lys Pro Arg Ser Lys Ser Ala Asp Lys Lys Pro Glu Glu Leu	
tct gta act ctt gta gag gca tac aca gat gtg ttt gat gac aca cag	1104
Ser Val Thr Leu Val Glu Ala Tyr Thr Asp Val Phe Asp Asp Thr Gln	
gtt gag atg att gat gag gtt acg aac taa (SEQ ID NO: 1)	1134
Val Glu Met Ile Asp Glu Val Thr Asn * (SEQ ID NO: 2)	

FIG. 1

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KU-2	MATQGORVNWGDEPSKRDRSNGRKNNIPLSFFNPTTLEQGAFWYVCPDRFVPKIGNKQQIGYWNQARFIVKGORKELPERWFFYELGTGPH	100
BlackG.....Y.I..S.S..NI.....V.Y..R.....S.....	100
UCD1G.....V.....D.....YY.I..QP.S..N.....Y.....	100
FIPV IIG.....D.....Y.I..S..NL..L.....I.Y.....A.....	100
FECV IIG.....D.....Y.I..D.S..NL.....Y.....V.....	100
CCV	..S...ST..G.....D.....I.....S..DL.....T.Y.M..R..N..K..Y.....	100
TGEV	..N...S...ST..T.G.....I..Q..S..NL.....R.....T.Y.M.....Y.....	100
KU-2	ADAKFKDKIDGVFWAKDGMNKPTSLGTRGTNNESEPLRFDKIPPOFQLEWRSRNRSGSRSGSRNRSQSRGR-QQNNQNTNVEDTIVAVLQK	199
BlackR.....T.....K.K.....K.L.....P.V..S.....S.....	199
UCD1R.....T.....K.L.....V.....F.....ND.....	199
FIPV IIR.....T.....K.....V.....-HH..N.....B.....	199
FECV IIA.....R.....K.K.....V.....	199
CCVQ.L..V..RGDS.T..T.....KA.K..V.V.SE.H...QL.D..R...Q.....QLSN.KKDD...QAVL.A.K..	200
TGEVL..V.....T.S.A...KA.K...V.GE.....Q.D..R...R.....Q.FN.KKDD.S..QAVL.A.K..	200
KU-2	LGV-TDK-QRSRSKSRDRSDSKSRDTPKANKHTWKTAGKDVTFEGARSANFGSDLVANGNAKCPQIAECVPSSVLFSGSQAEEAGD	296
BlackGE.NQ..P.....Y...S.....A..I.....	296
UCD1S.....E..QL.....R.....Y.....L.....	296
FIPV IIP.E.....P.....TY..S.....II.....	296
FECV IIGE.Q.....Y...S.....I.....	296
CCV	..D.E.-Q.....KE.S..T.....E.....R.....K.Y..S.....G.H..L.....I...H.T.K.D..	299
TGEV	..D.E.QQ.....KE.N.T.....E...S.R.....R.Y..S...T...SS.H..L.....I...Y.TSK.D..	300
KU-2	QVKVTLTHTYLPGDAKTSQFLEQIDAYKRPSQVAKQRPKRPSKSGADKKPEE-LSVTLVEAYTDVDDTQVEMIDEVTN (SEQ ID NO: 2)	377
BlackD.....Q.E..D..QR.S.....	377
UCD1D.....E..D..SR.S.....	377
FIPV IID.....E..D..QRS.....	377
FECV IIN.....D.....E..D..QR.S.....	376
CCV	..IE..F..K.H..D.P..G..Q..N..A..E.....QR.A...VERVEQ.VPDA.T.N.....I.....	381
TGEV	..IE..F..K.H..D.P..G..Q..N..A..E.....R.S...ERSEQDVPA.I.N.....I.....	382

FIG. 2

N GENE

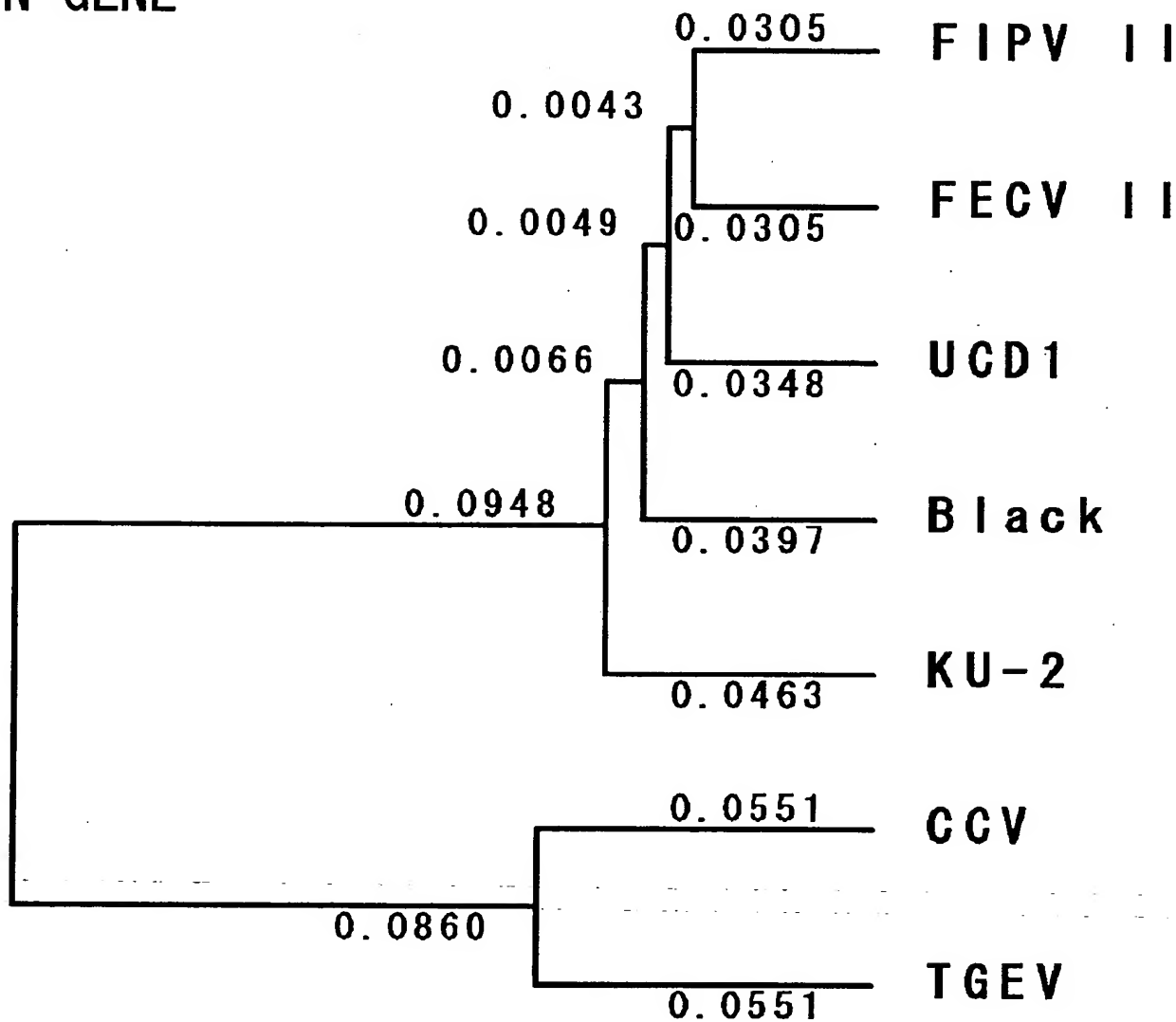


FIG. 3

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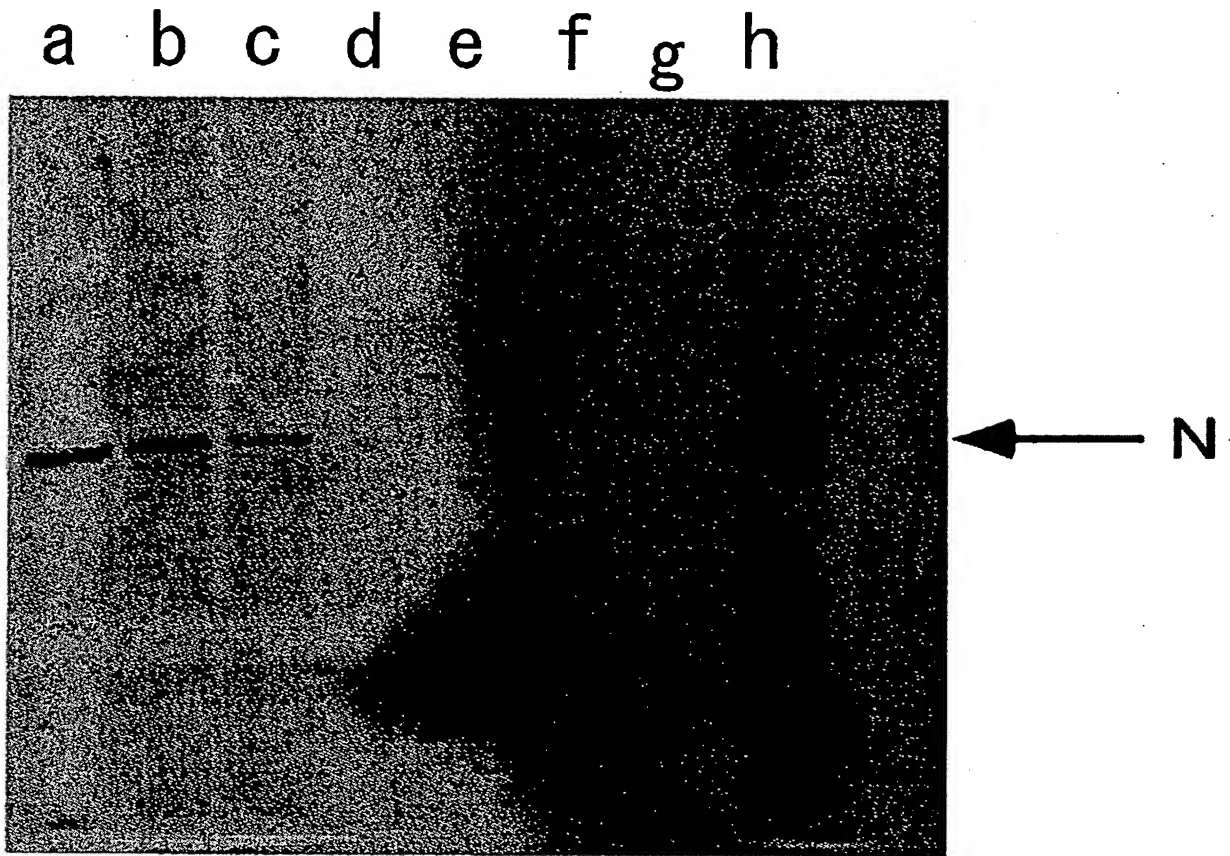


FIG. 4

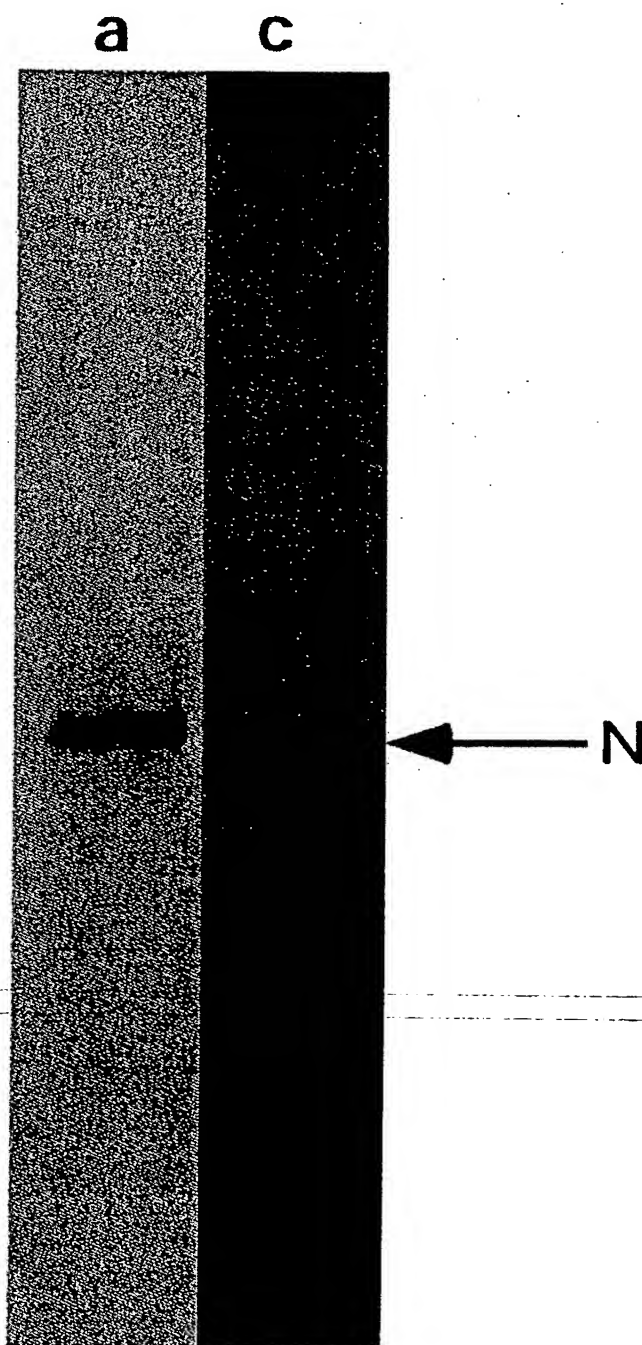


FIG. 5

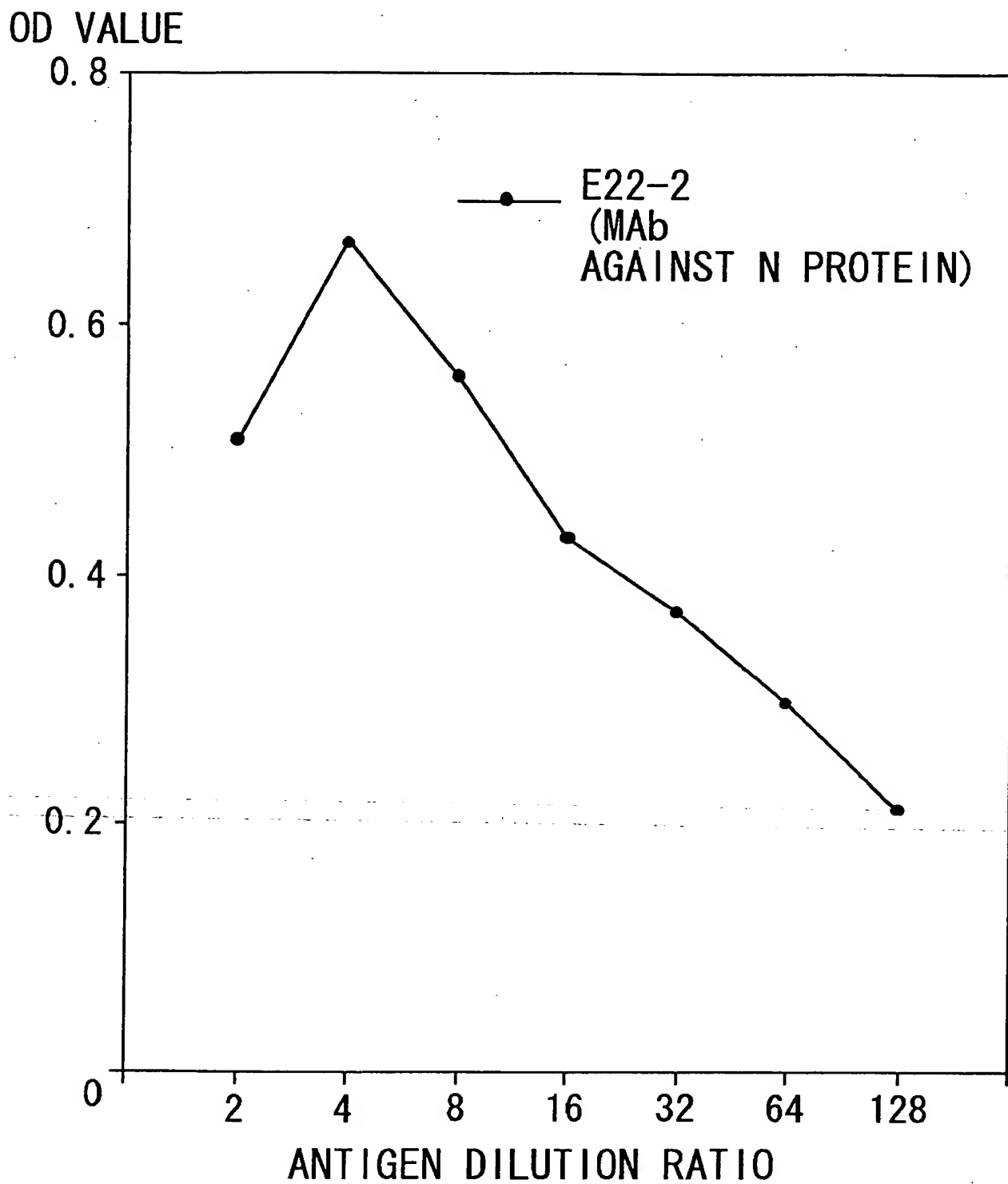


FIG. 6

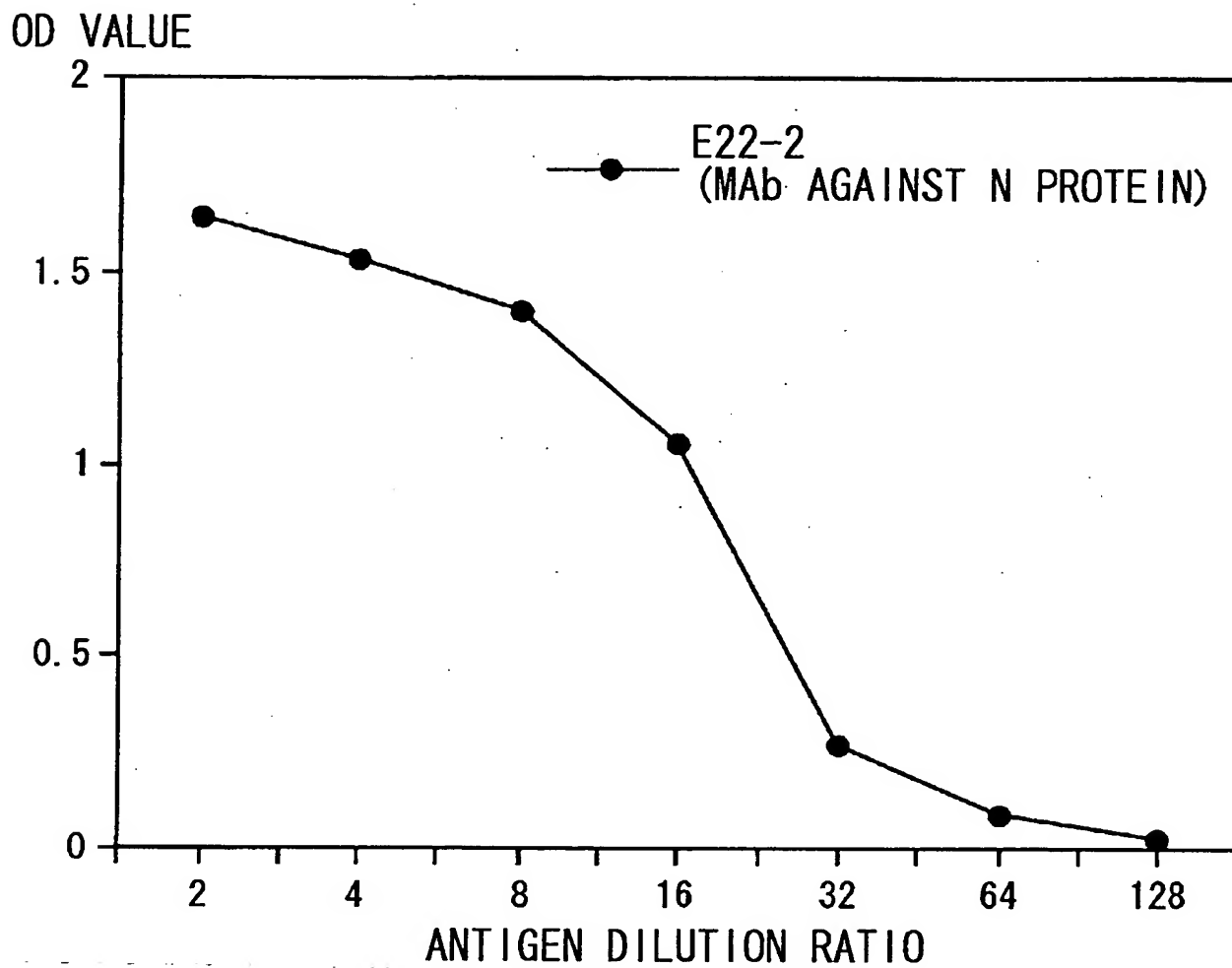
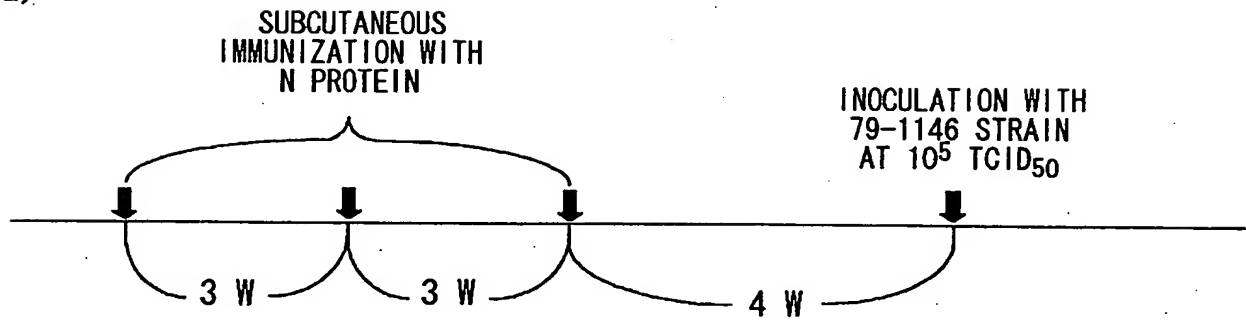


FIG. 7

(a)



(b)

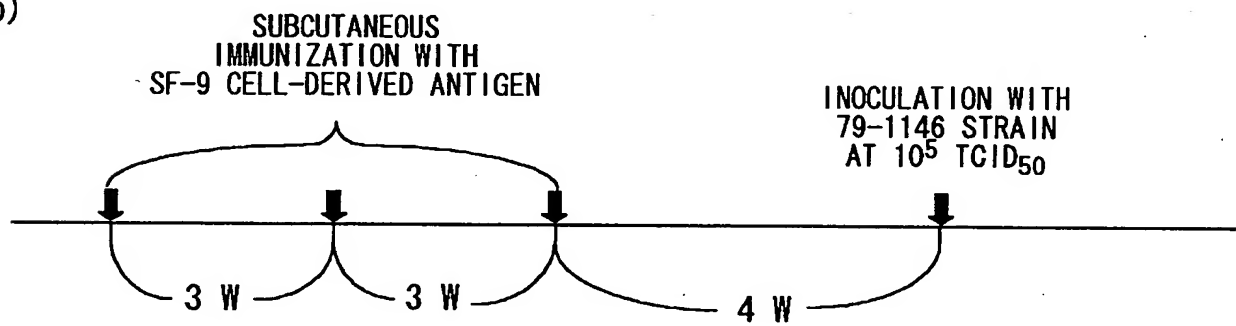


FIG. 8

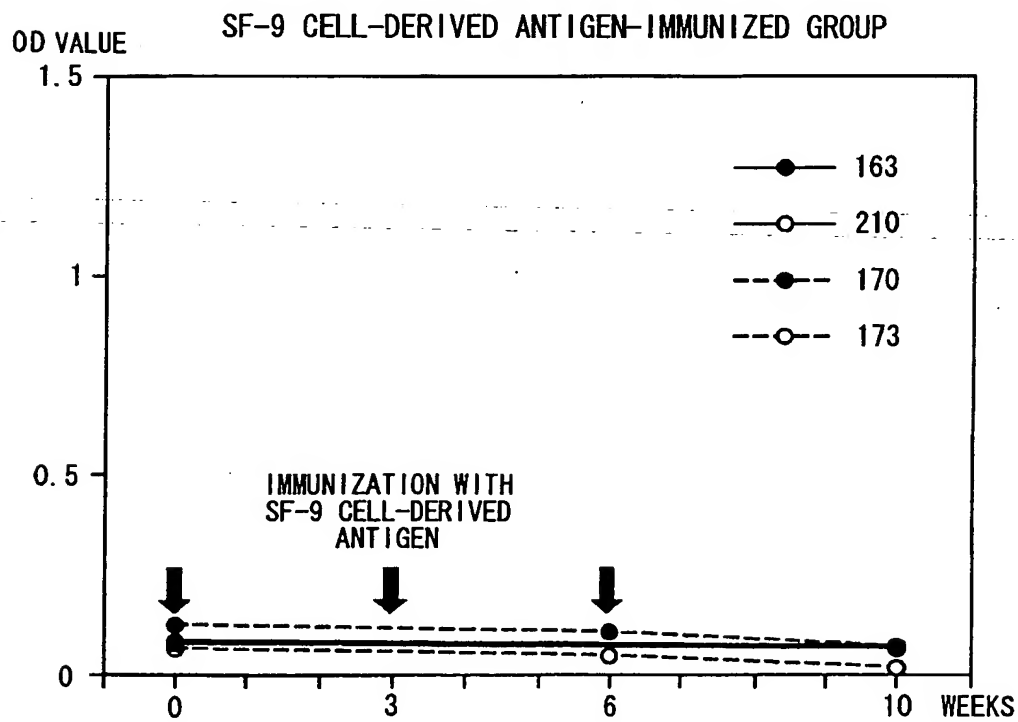
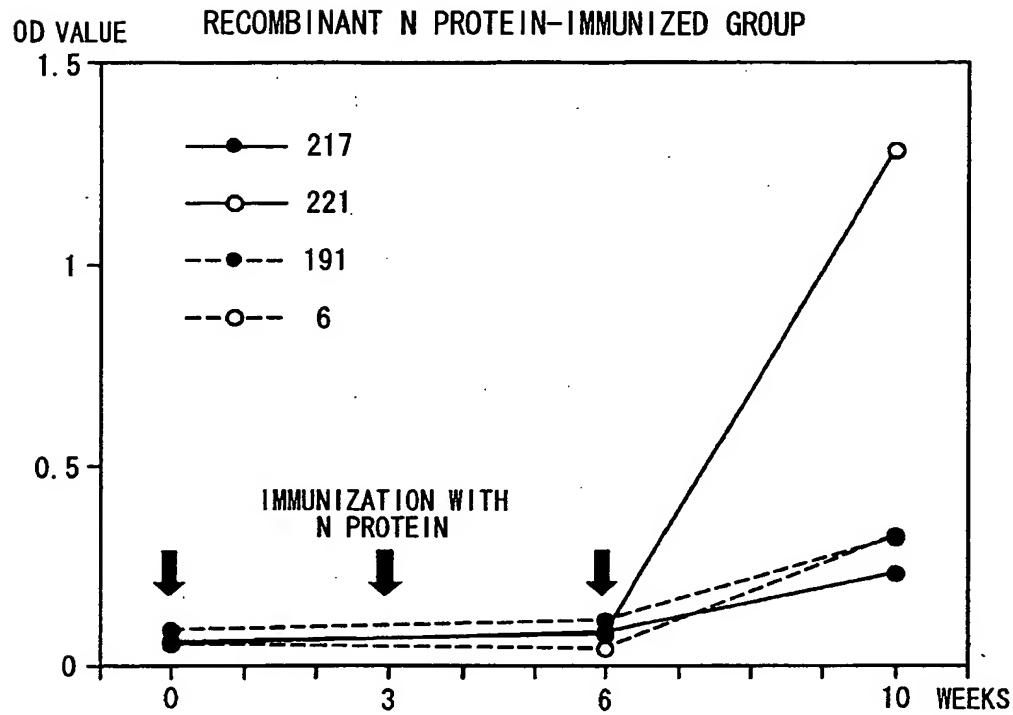


FIG. 9

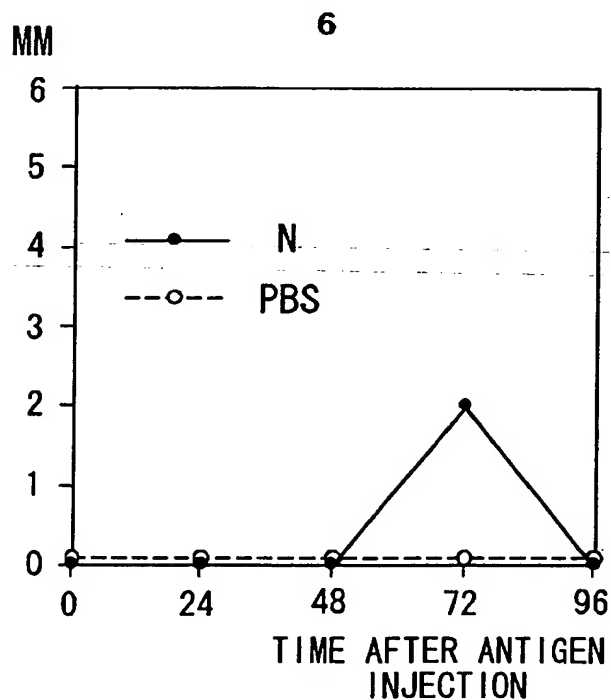
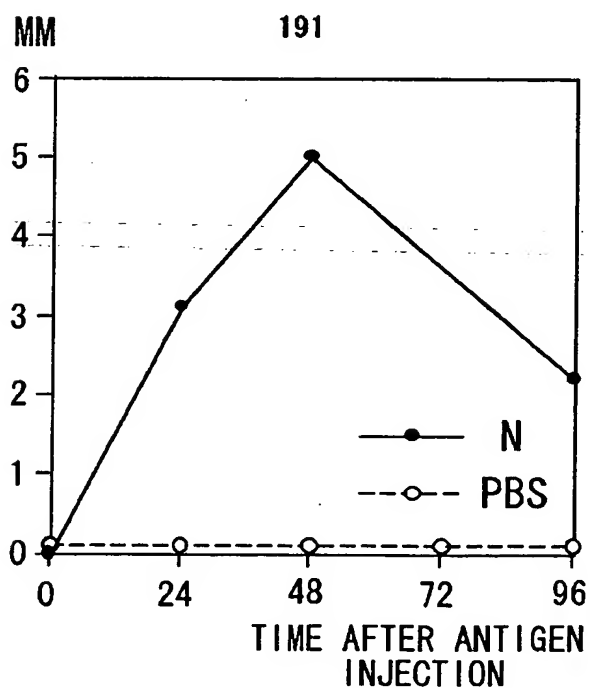
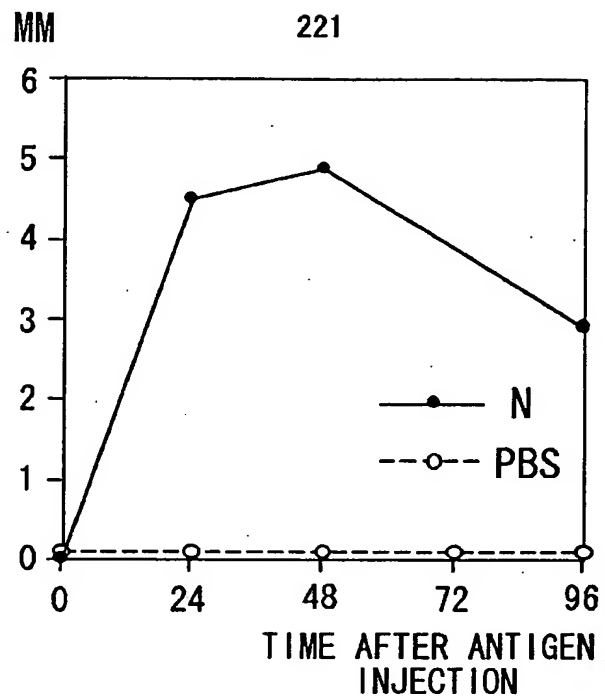
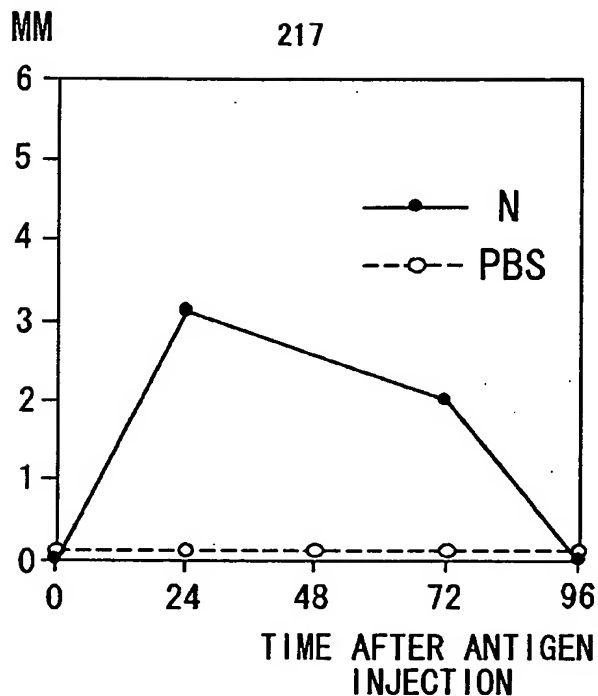


FIG. 10

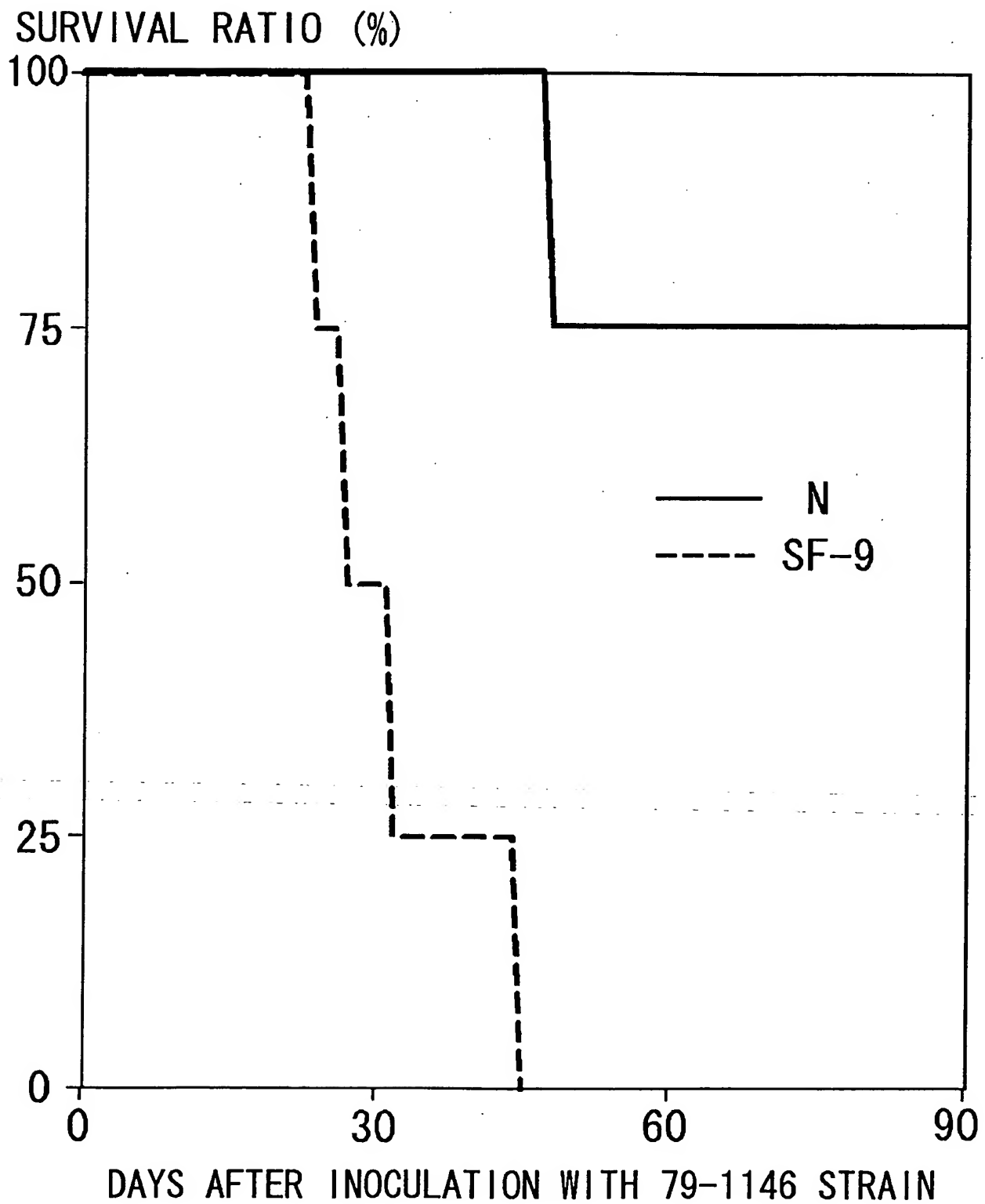


FIG. 11

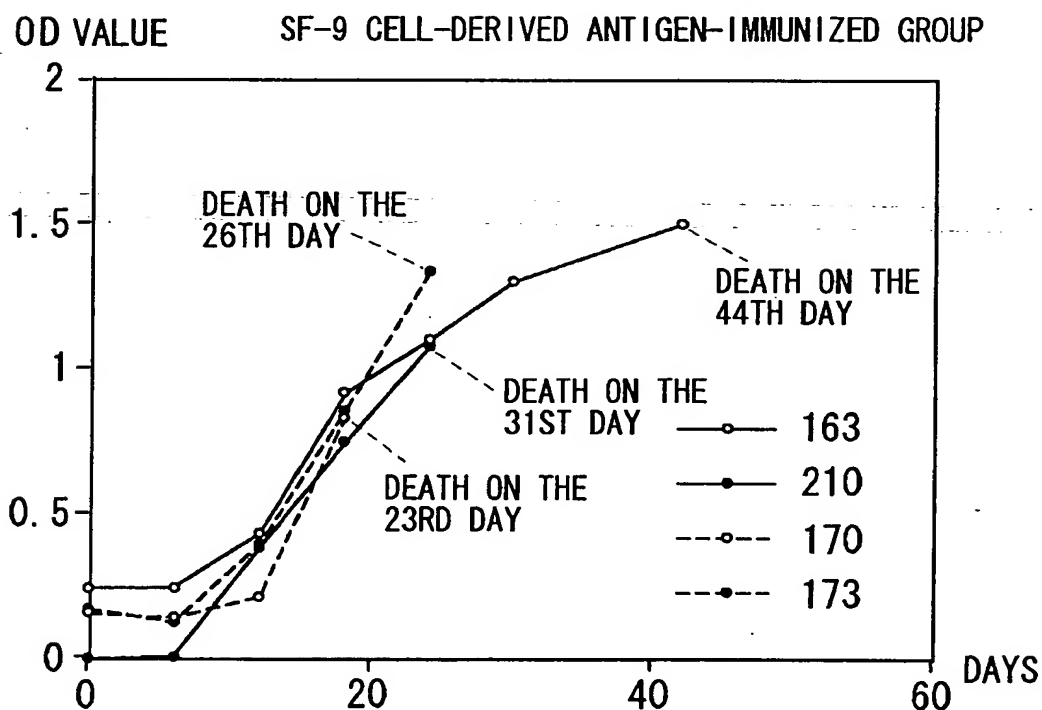
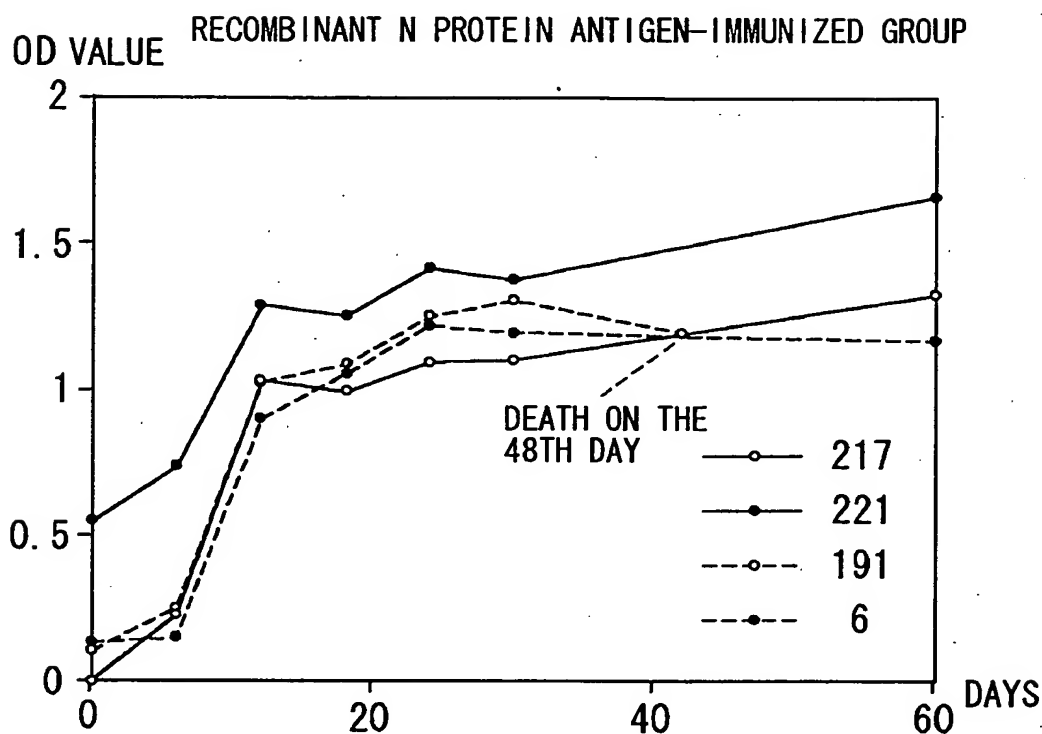


FIG. 12

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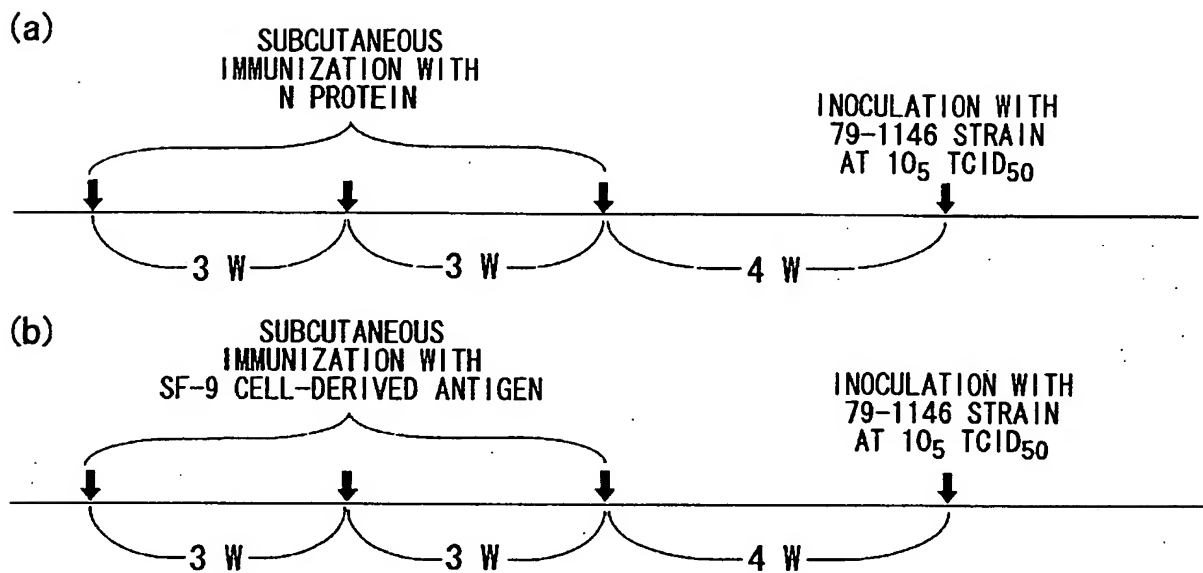


FIG. 13

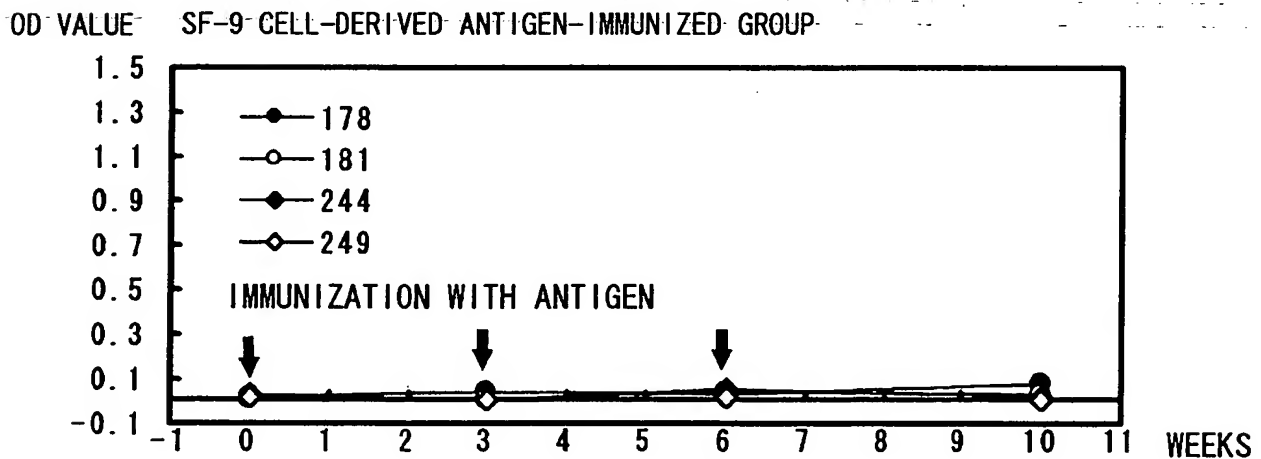
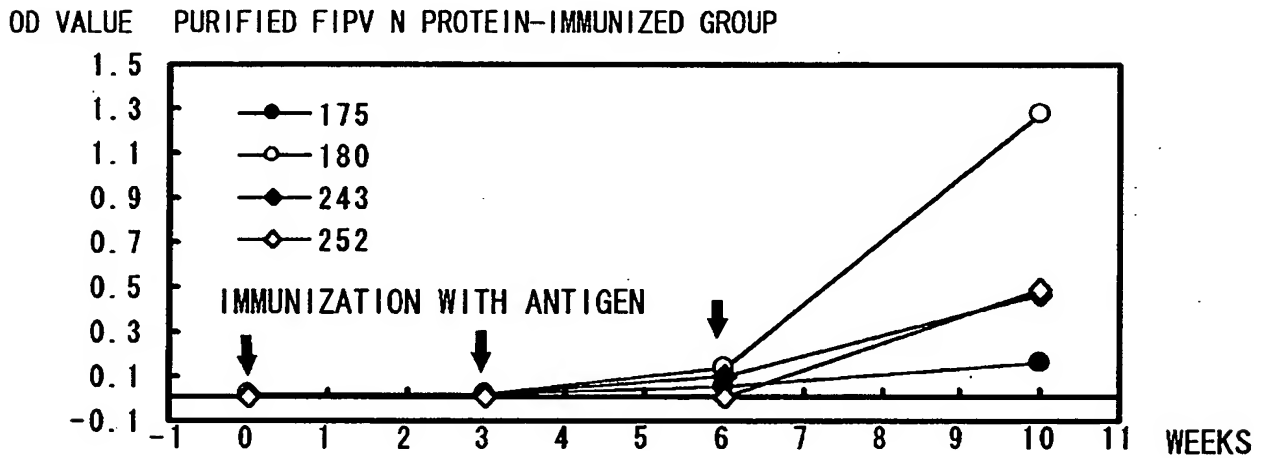
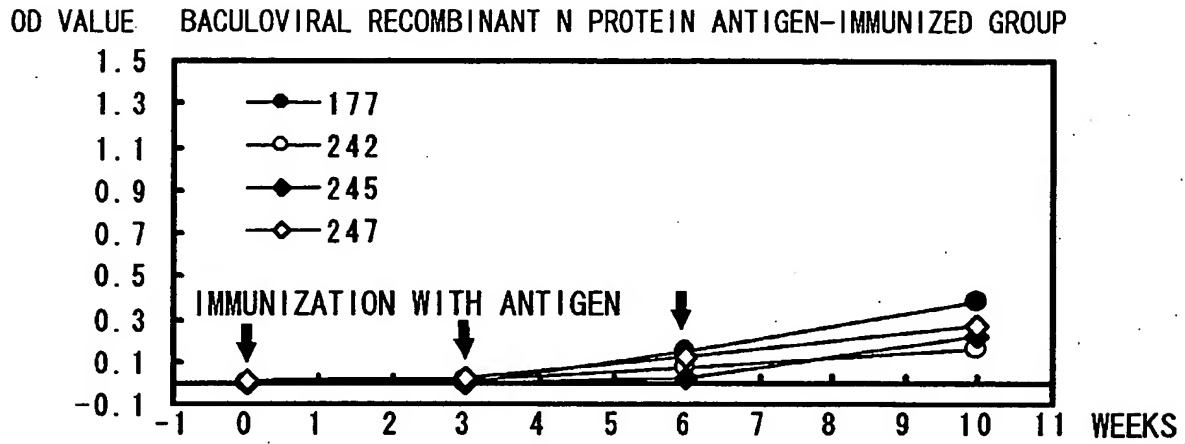


FIG. 14

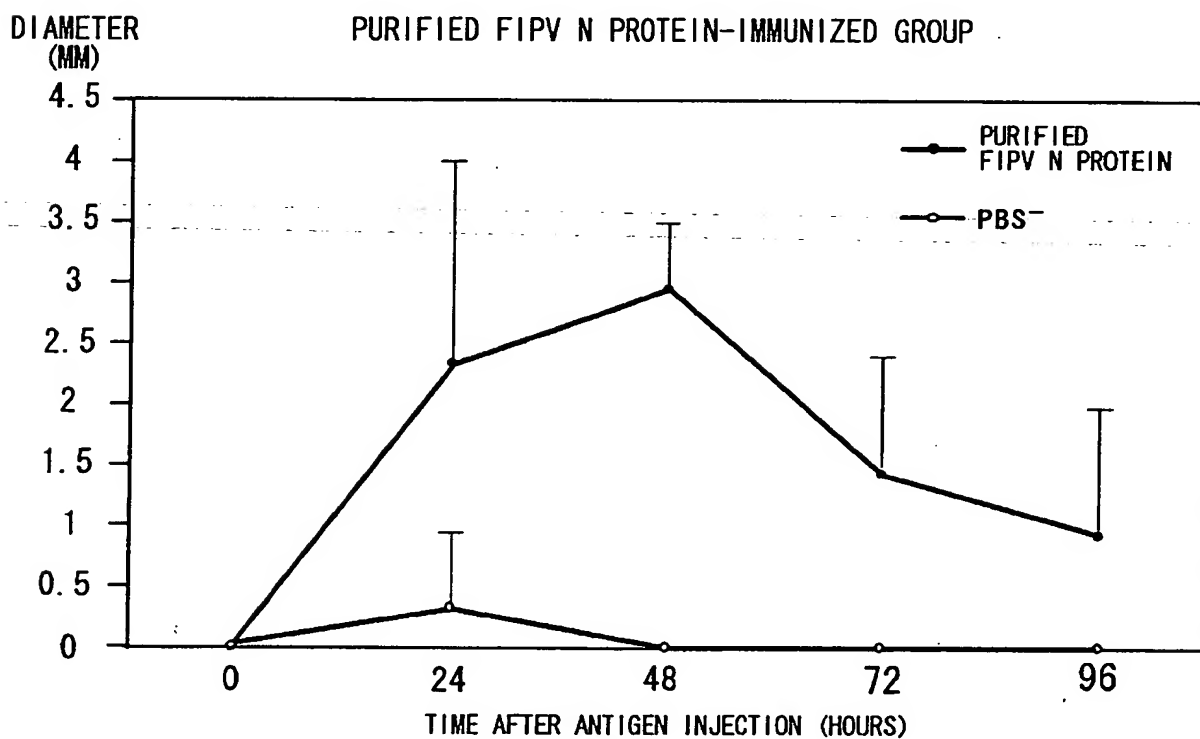
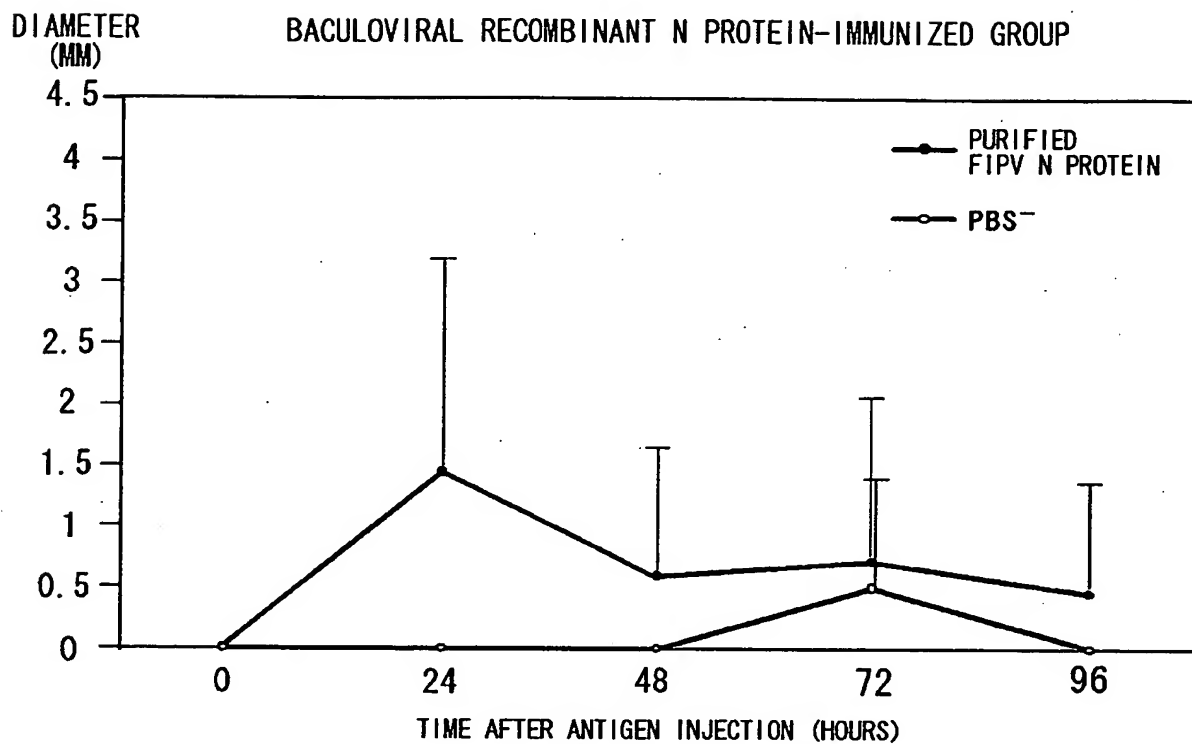


FIG. 15

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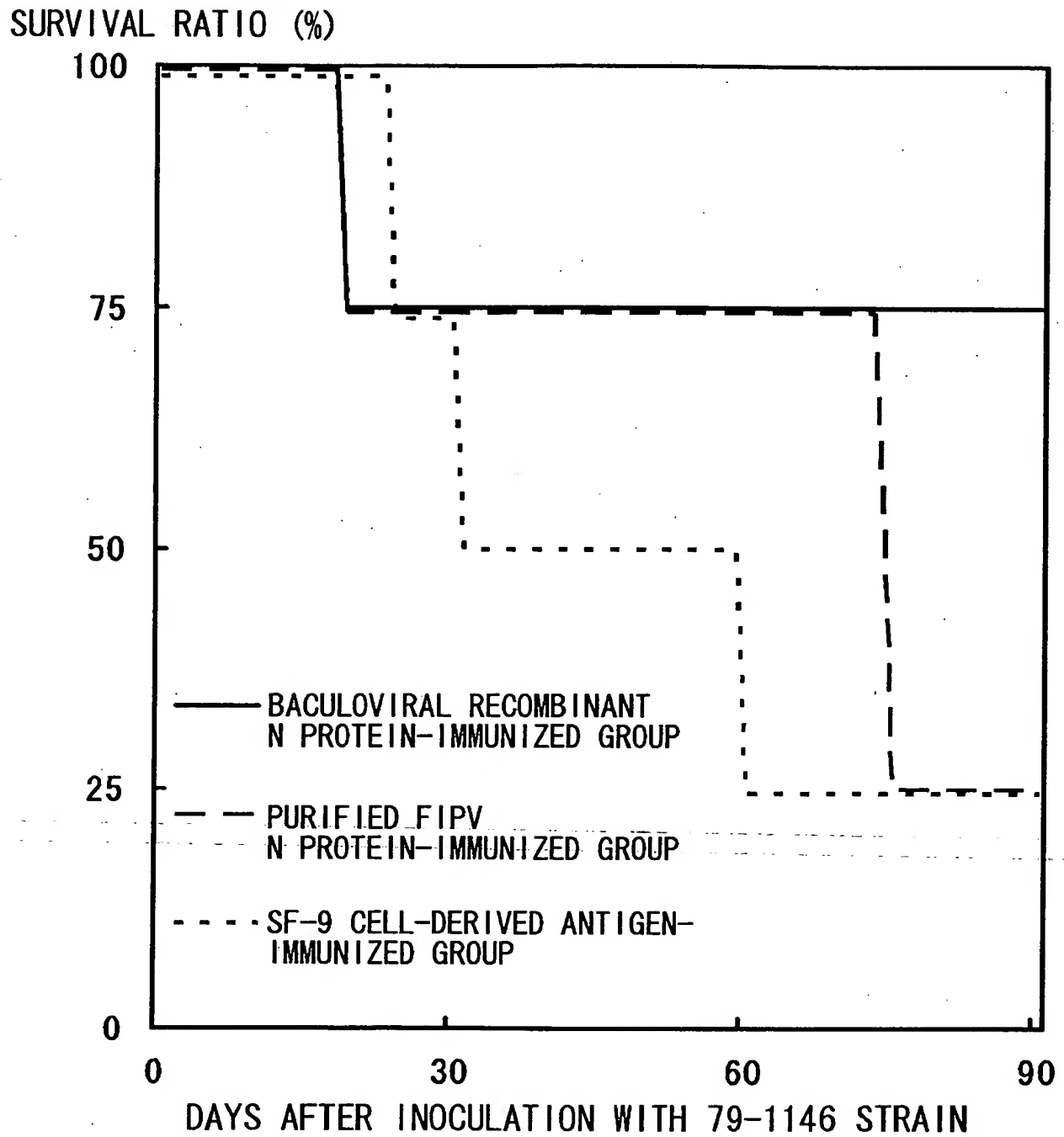


FIG. 16

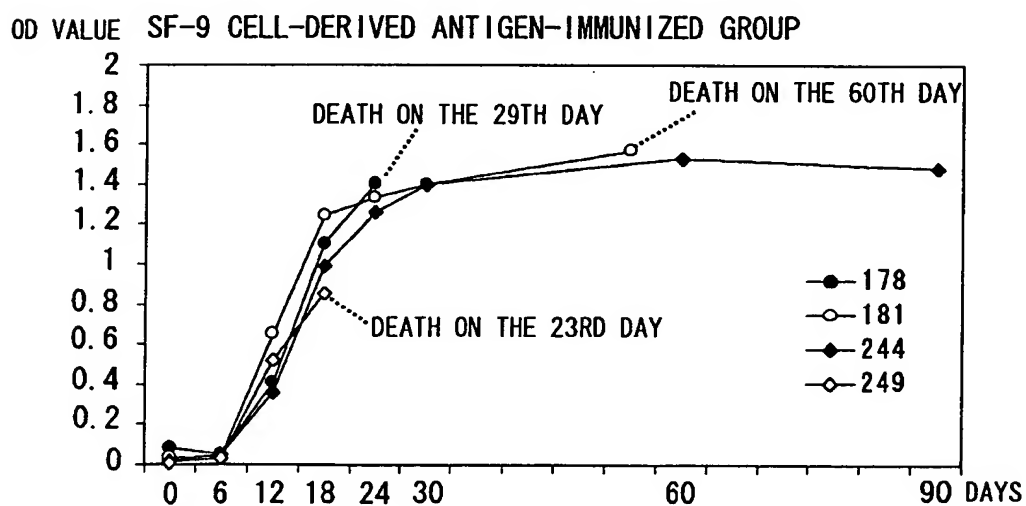
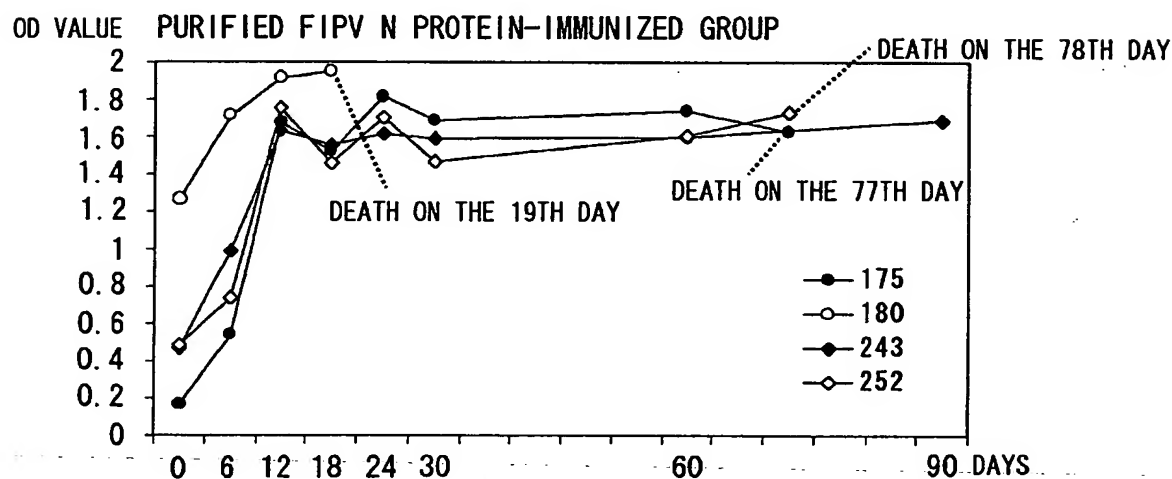
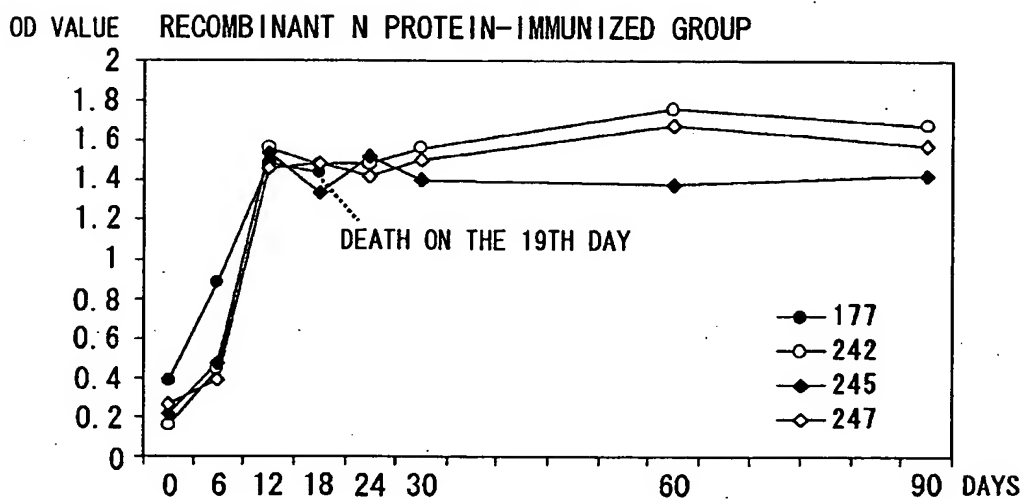


FIG. 17

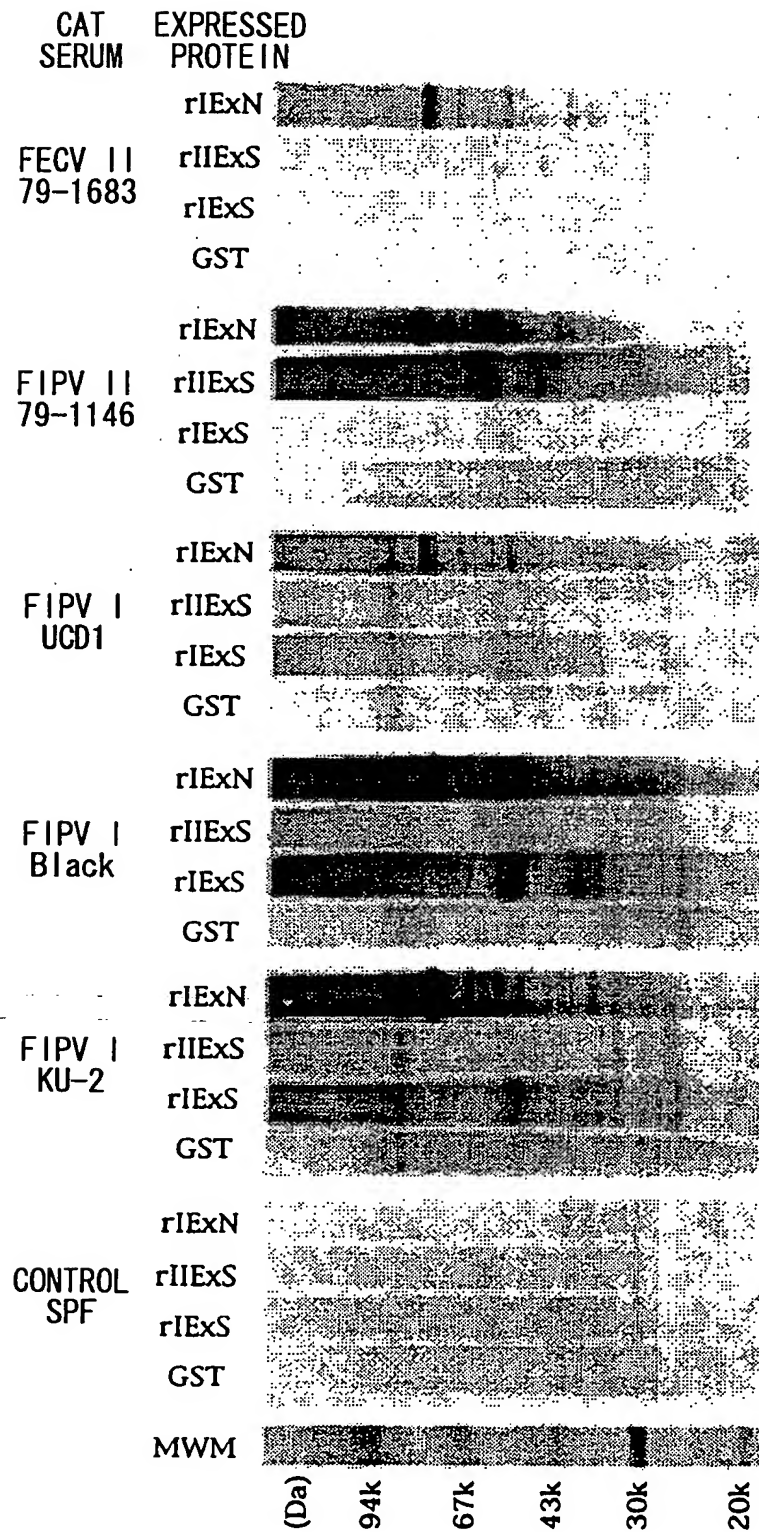


FIG. 18

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